

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- 5 (A) NAME:
ASAT AG Applied Science & Technology
(B) STREET: Baarerstrasse 77
(C) CITY: Zug
(E) COUNTRY: Switzerland
10 (F) POSTAL CODE: 6302

(ii) TITLE OF INVENTION: Recombinant antibodies

(iii) NUMBER OF SEQUENCES: 30

(iv) COMPUTER-READABLE FORM:

- 15 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: PatentIn Release #1.0,
Version #1.30 (EPO)

(vi) ORIGINAL APPLICATION DATA:

- 25 (A) APPLICATION NUMBER: DE 19723904.8
(B) APPLICATION DATE: 06-JUN-1997

(vi) ORIGINAL APPLICATION DATA:

- 30 (A) APPLICATION NUMBER: DE 19755227.7
(B) APPLICATION DATE: 12-DEC-1997

(vi) ORIGINAL APPLICATION DATA:

- 35 (A) APPLICATION NUMBER: DE 19820663.1
(B) APPLICATION DATE: 08-MAY-1998

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs

SECRET - INFORMATION

- (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) NOTATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAG GTG AAA CTG CTC GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG 48
 Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

ACC CTG TCC CTC AAC TGC ACT GTC TCT GGT CGC TCC ATC AGT GGT TAC 96
 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
 20 25 30

TCT TGG AGA TGG ATC CGG CAG TCT CCA GGG AAG GGA CTA GAG TGG ATT 144
 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

GGG GAT ATC TCT TAT AGT GGG AGT ACC AAG TAC AAA CCG TCC CTC AGG 192
 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
 50 55 60

AGT CGA GTC ACC CTG TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG 240
 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

AAG CTG AAT TCG GTG ACC GCT GCG GAC ACG GCC GTC TAT TAC TGT GCG 288
 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

CGA GTC TTG CCC TTT GAC CCG ATC TCG ATG GAC GTC TGG GGC AAA GGG 336
 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
 100 105 110

ACC ACG GTC ACC GTC TCC TCA 357
 Thr Thr Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
 20 25 30
 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
 50 55 60
 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGG CAG TGG GTC 48
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val
 120 125 130 135
 ACC ATC TCT TGT TCT GGG AGC AGC TCC AAC ATC AGA AGT AAT CCT GTT 96
 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
 140 145 150
 AGC TGG TAT CAC CAG GTC CCA GGC ACG GCC CCC AAA CTC CTC ATC TTT 144
 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
 155 160 165
 GGT AGT CAT CAG CGG CCC TCA GGG GTC CCT GAC CGA TTC TCT GGC TCC 192
 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 170 175 180
 AAG TCG GGC ACC TCC GCC TCC CTG GCC ATC CGT GGG CTC CAA TCT GGG 240
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
 185 190 195

Sequence: 333 bp

15

GAT GCT GGT GAC TAT TAC TGT GCA ACA TGG GAT GAC GGC CTC AAT GGT 288
 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly 215
 200 205 210
 CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC 333
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 230
 220 225

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val 15
 1 5 10
 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val 30
 20 25 30
 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe 45
 35 40 45
 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser 60
 50 55 60
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly 80
 65 70 75 80
 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly 95
 85 90 95
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 110
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 369 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 115 120 125
 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 130 135 140
 GCT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 145 150 155
 GCA GTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG 192
 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 160 165 170 175
 AAG GGC CGA TTC GCC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT 240
 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 180 185 190
 CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 195 200 205
 GCG AGA GCG CTG GGG AGC TGG GGG GGT TGG GAC CAC TAC ATG GAC GTC 336
 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
 210 215 220
 TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 369
 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 225 230

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
 100 105 110
 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGG CAG AGG GTC 48
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 125 130 135

ACC ATC TCT TGT TCT GGA AGC AGC TCC AAC ATC GGA AGT AAT ACT GTA 96
 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
 140 145 150 155

AAC TGG TAC CAG CAG CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT 144
 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 160 165 170

AGT AAT AAT CAG CGG CCC TCA GGG GTC CCT GAC CGA TTC TCT GGC TCC 192
 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 175 180 185

AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC AGT GGG CTC CAG TCT GAG 240
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
 190 195 200

GAT GAG GCT GAT TAT TAC TGT GCA GCA TGG GAT GAC AGC CTG AAT GGT 288
 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
 205 210 215

TGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT CAG CCC 333
 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 220 225 230

15 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Val	Val	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln	Arg	Val
1				5					10					15	
Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn	Ile	Gly	Ser	Asn	Thr	Val
			20					25					30		
Asn	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
		35					40					45			
Ser	Asn	Asn	Gln	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	50						55				60				
Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Ser	Gly	Leu	Gln	Ser	Glu
65					70					75					80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Ala	Trp	Asp	Asp	Ser	Leu	Asn	Gly
				85					90					95	
Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO: 9:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (ix) FEATURE:

- ```
(A) NAME/KEY: CDS
(B) LOCATION: 1..369
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15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAG | GTG | AAA | CTG | CTC | GAG | TCT | GGG | GGA | GGC | TTG | GTT | CAC | CCC | GGG | GGG | 48  |
| Gln | Val | Lys | Leu | Leu | Glu | Ser | Gly | Gly | Gly | Leu | Val | His | Pro | Gly | Gly |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| TCC | CTG | AGA | CTC | TCT | TGT | GCA | GCC | TCT | GGA | TTT | ACG | TTT | GAC | AAC | TTT | 96  |
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Asp | Asn | Phe |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| GCC | ATG | AGC | TGG | GTC | CGC | CAG | GCT | CCA | GGG | AAG | GGG | CTG | GAG | TGG | GTC | 144 |
| Ala | Met | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |     |
|     |     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |
| TCA | GGC | ATT | AGT | GGT | GGT | GGT | CTT | TTG | ACA | CAC | TAC | GCA | GAC | TCC | GTG | 192 |
| Ser | Gly | Ile | Ser | Gly | Gly | Gly | Leu | Leu | Thr | His | Tyr | Ala | Asp | Ser | Val |     |
| 160 |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| AAG | GGC | CGG | TTC | ACC | ATC | TCC | AGA | AAC | AAT | TCC | AGG | AAC | ACT | GTA | TAC | 240 |
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asn | Asn | Ser | Arg | Asn | Thr | Val | Tyr |     |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| CTA | CAA | ATG | AAC | AGC | CTG | AGA | GCC | GAA | GAC | ACG | GCC | GTG | TAT | TAT | TGT | 288 |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |     |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |

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GTG AGA GAT CTG GGC TAT AGA GTA CTT TCG ACT TTT ACT TTT GAT ATC 336  
 Val Arg Asp Leu Gly Tyr Arg Val Leu Ser Thr Phe Thr Phe Asp Ile  
           210                                  215                                  220

TGG GGC CAG GGG ACA AAG GTC ACC GTC TCT TCA 369  
 Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser  
           225                                  230

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 123 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly  
   1                  5                                  10                                  15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe  
                   20                                  25                                  30  
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                  40                                  45  
 Ser Gly Ile Ser Gly Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val  
           50                                  55                                  60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr  
   65                                  70                                  75                                  80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95  
 Val Arg Asp Leu Gly Tyr Arg Val Leu Ser Thr Phe Thr Phe Asp Ile  
                   100                                  105                                  110  
 Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser  
           115                                  120

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..375

Sequence of the protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTG | GTG | ACT | CAG | CCT | GCC | TCC | GTG | TCT | GGG | TCT | CCT | GGA | CAG | TCG | ATC | 48  |
| Val | Val | Thr | Gln | Pro | Ala | Ser | Val | Ser | Gly | Ser | Pro | Gly | Gln | Ser | Ile |     |
| 125 |     |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     |
| ACC | ATC | TCC | TGC | ACT | GGA | ACC | AGC | AGT | GCT | ATT | GGG | AAT | TAT | AAC | TTT | 96  |
| Thr | Ile | Ser | Cys | Thr | Gly | Thr | Ser | Ser | Ala | Ile | Gly | Asn | Tyr | Asn | Phe |     |
| 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |
| GTC | CCC | TGG | TAC | CAA | CAG | CAC | CCA | GGC | AAA | GCC | CCC | AAA | CTC | ATG | ATT | 144 |
| Val | Pro | Trp | Tyr | Gln | Gln | His | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Met | Ile |     |
|     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |
| TAT | GAG | GGC | AGT | AAG | CGG | CCC | TCA | GGG | GTT | TCT | AAT | CGC | TTC | TCT | GGC | 192 |
| Tyr | Glu | Gly | Ser | Lys | Arg | Pro | Ser | Gly | Val | Ser | Asn | Arg | Phe | Ser | Gly |     |
|     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |
| TCC | AAG | TCT | GGC | AAC | ACG | GCC | TCC | CTG | ACA | ATC | TCT | GGG | CTC | CAG | GCT | 240 |
| Ser | Lys | Ser | Gly | Asn | Thr | Ala | Ser | Leu | Thr | Ile | Ser | Gly | Leu | Gln | Ala |     |
|     |     |     | 190 |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     |
| GAG | GAC | GAG | GCT | GAG | TAT | TAC | TGC | TGC | TCA | TAT | GTT | CAT | AGT | AGC | ACT | 288 |
| Glu | Asp | Glu | Ala | Glu | Tyr | Tyr | Cys | Cys | Ser | Tyr | Val | His | Ser | Ser | Thr |     |
| 205 |     |     |     |     | 210 |     |     |     |     |     | 215 |     |     |     |     |     |
| AAT | TGG | GTG | TTC | GGC | GGA | GGG | ACC | AAG | CTG | ACC | GTC | CTA | GGT | CAG | CCC | 336 |
| Asn | Trp | Val | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Thr | Val | Leu | Gly | Gln | Pro |     |
| 220 |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |
| AAG | GCT | GCC | CCC | TCG | GTC | ACT | CTG | TTC | CCA | CCC | TCC | TCT |     |     |     | 375 |
| Lys | Ala | Ala | Pro | Ser | Val | Thr | Leu | Phe | Pro | Pro | Ser | Ser |     |     |     |     |
|     |     |     | 240 |     |     |     |     | 245 |     |     |     |     |     |     |     |     |

## 5 (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Thr | Gln | Pro | Ala | Ser | Val | Ser | Gly | Ser | Pro | Gly | Gln | Ser | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ile | Ser | Cys | Thr | Gly | Thr | Ser | Ser | Ala | Ile | Gly | Asn | Tyr | Asn | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Pro | Trp | Tyr | Gln | Gln | His | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Met | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Glu | Gly | Ser | Lys | Arg | Pro | Ser | Gly | Val | Ser | Asn | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Ser | Lys | Ser | Gly | Asn | Thr | Ala | Ser | Leu | Thr | Ile | Ser | Gly | Leu | Gln | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Asp | Glu | Ala | Glu | Tyr | Tyr | Cys | Cys | Ser | Tyr | Val | His | Ser | Ser | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro  
 100 105 110  
 Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 10 (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..366

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

15 CAG GTG AAA CTG CTC GAG TCA GGA CCA GGA CTG GTG AAG CCC TCG GAG 48  
 Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 130 135 140  
 ACC CTG TCT CTC ACC TGC ACT GTC TCT GAT GTC TCC ATC AGA AGT CAT 96  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Val Ser Ile Arg Ser His  
 145 150 155  
 TAC TGG AGT TGG CTC CGG CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT 144  
 Tyr Trp Ser Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 160 165 170  
 GGG TTT ATC TAT GAC GGT GCG AGA ACC AGG TTC AAC CCC TCC CTC AGG 192  
 Gly Phe Ile Tyr Asp Gly Ala Arg Thr Arg Phe Asn Pro Ser Leu Arg  
 175 180 185  
 AGT CGA GTC TCC CTT TCA ATG GAC CCA TCC AAG AAG CAG TTT TCC CTG 240  
 Ser Arg Val Ser Leu Ser Met Asp Pro Ser Lys Lys Gln Phe Ser Leu  
 190 195 200 205  
 AAA CTG GGG TCT GTG ACC GCT GCG GAC TCG GCC GTC TAC TAC TGT GCG 288  
 Lys Leu Gly Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala  
 210 215 220  
 AGA GAC GCG GAT GGA GAT GGC TTC AGC CCA TAC TAC TTT CCC TAC TGG 336  
 Arg Asp Ala Asp Gly Asp Gly Phe Ser Pro Tyr Tyr Phe Pro Tyr Trp  
 225 230 235  
 GGC CAG GGA ATC CCG GTC TCC GTC TCC TCG 366  
 Gly Gln Gly Ile Pro Val Ser Val Ser Ser  
 240 245

## (2) INFORMATION FOR SEQ ID NO: 14

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 122 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Val Ser Ile Arg Ser His  
 20 25 30  
 Tyr Trp Ser Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Phe Ile Tyr Asp Gly Ala Arg Thr Arg Phe Asn Pro Ser Leu Arg  
 50 55 60  
 Ser Arg Val Ser Leu Ser Met Asp Pro Ser Lys Lys Gln Phe Ser Leu  
 65 70 75 80  
 Lys Leu Gly Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 Arg Asp Ala Asp Gly Asp Gly Phe Ser Pro Tyr Tyr Phe Pro Tyr Trp  
 100 105 110  
 Gly Gln Gly Ile Pro Val Ser Val Ser Ser  
 115 120

5 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAC CCT GGG AGG 48  
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val His Pro Gly Arg  
 125 130 135  
 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 140 145 150  
 ACT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144  
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 155 160 165 170  
 GCA CTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTC 192  
 Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 175 180 185

- 60 -

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAG GGC CGA TTC GCC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTA TAT | 240 |
| Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr |     |
| 190 195 200                                                     |     |
| CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT | 288 |
| Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys |     |
| 205 210 215                                                     |     |
| GCG AAA GAT GGC CGG AGT GGG AGC TAC GCC AGG TTC GAC GGT ATG GAC | 336 |
| Ala Lys Asp Gly Arg Ser Gly Ser Tyr Ala Arg Phe Asp Gly Met Asp |     |
| 220 225 230                                                     |     |
| GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA                 | 372 |
| Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser                 |     |
| 235 240 245                                                     |     |

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val His Pro Gly Arg | 15  |
| 1 5 10                                                          |     |
| Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr | 30  |
| 20 25 30                                                        |     |
| Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val | 45  |
| 35 40 45                                                        |     |
| Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val | 60  |
| 50 55 60                                                        |     |
| Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr | 80  |
| 65 70 75 80                                                     |     |
| Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys | 95  |
| 85 90 95                                                        |     |
| Ala Lys Asp Gly Arg Ser Gly Ser Tyr Ala Arg Phe Asp Gly Met Asp | 110 |
| 100 105 110                                                     |     |
| Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser                 |     |
| 115 120                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..372

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTA CAG CCT GGC AGG | 48  |
| Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg |     |
| 125 130 135 140                                                 |     |
| TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT GAT GAT TAT | 96  |
| Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr |     |
| 145 150 155                                                     |     |
| GCC CTG CAC TGG GTC CGT CAA GCT CCA GGG AAG GGC CTG GAG TGG GTC | 144 |
| Ala Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val |     |
| 160 165 170                                                     |     |
| TCA GGT ATT AGT TGG GAT AGT GGT ACC ATA GGC TAT GCG GAC TCT GTG | 192 |
| Ser Gly Ile Ser Trp Asp Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val |     |
| 175 180 185                                                     |     |
| AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC TCC CTG TAT | 240 |
| Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr |     |
| 190 195 200                                                     |     |
| CTG CAA ATG AAC AGT CTG AGA GCT GAG GAC ACG GCC TTG TAT TAC TGT | 288 |
| Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys |     |
| 205 210 215 220                                                 |     |
| GTA AAA GAT ATG GGG TCT TCG GTA GTG GCT ACG TAC AAT GCT TTT GAT | 336 |
| Val Lys Asp Met Gly Ser Ser Val Val Ala Thr Tyr Asn Ala Phe Asp |     |
| 225 230 235                                                     |     |
| ATC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA                 | 372 |
| Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser                 |     |
| 240 245                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg |  |
| 1 5 10 15                                                       |  |
| Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr |  |
| 20 25 30                                                        |  |
| Ala Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val |  |
| 35 40 45                                                        |  |
| Ser Gly Ile Ser Trp Asp Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val |  |
| 50 55 60                                                        |  |
| Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr |  |
| 65 70 75 80                                                     |  |

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys  
                                     85                                    90                                    95

Val Lys Asp Met Gly Ser Ser Val Val Ala Thr Tyr Asn Ala Phe Asp  
                                     100                                    105                                    110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser  
                                     115                                    120

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA for mRNA

(vii) IMMEDIATE SOURCE:

(B) CLONE(E): AI-X2

15 (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

|                                                                                                                          |     |
|--------------------------------------------------------------------------------------------------------------------------|-----|
| CAG GTG AAA CTG CTC GAG TCA GGC CCA GGA CTG GTG AAG CCT TCG GAG                                                          | 48  |
| Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu                                                          |     |
| 125                                    130                                    135                                    140 |     |
| ACC CTG TCC CTC ACC TGC ACT GTC TCT GGT GGC TCC TTC AGT ACT TAC                                                          | 96  |
| Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr                                                          |     |
| 145                                    150                                    155                                        |     |
| TAT TGG AGC TGG ATC CGG CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT                                                          | 144 |
| Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile                                                          |     |
| 160                                    165                                    170                                        |     |
| GGG TAT ATC TAT TAC AGT GGG AAC ACC AAC TAC AAC CCC TCC CTC AAG                                                          | 192 |
| Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys                                                          |     |
| 175                                    180                                    185                                        |     |
| AGT CGA GCC ACC ATA TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG                                                          | 240 |
| Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu                                                          |     |
| 190                                    195                                    200                                        |     |
| AAG CTG AGC TCT GTT ACC GCC GCA GAC ACG GCC GTA TAT TAC TGT GCG                                                          | 288 |
| Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala                                                          |     |
| 205                                    210                                    215                                    220 |     |
| AGA CTG CGT AAC GAT GGC TGG AAT GAT GGC TTT GAT ATC TGG GGC CAA                                                          | 336 |
| Arg Leu Arg Asn Asp Gly Trp Asn Asp Gly Phe Asp Ile Trp Gly Gln                                                          |     |
| 225                                    230                                    235                                        |     |

GGG ACA ATG GTC ACC GTC TCT TCA  
 Gly Thr Met Val Thr Val Ser Ser  
 240

360

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 120 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr  
 20 25 30  
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60  
 Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80  
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 Arg Leu Arg Asn Asp Gly Trp Asn Asp Gly Phe Asp Ile Trp Gly Gln  
 100 105 110  
 Gly Thr Met Val Thr Val Ser Ser  
 115 120

## (2) INFORMATION FOR SEQ ID NO: 21

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 20 (ii) MOLECULE TYPE: cDNA for mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## 25 (vii) IMMEDIATE SOURCE:

(B) CLONE(E): AI-B14

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 14

5

(B) MAP POSITION: q32.3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..369

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG | 48  |
| Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg |     |
| 125 130 135                                                     |     |
| TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT GAC TAT | 96  |
| Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr |     |
| 140 145 150                                                     |     |
| GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG | 144 |
| Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val |     |
| 155 160 165                                                     |     |
| GCA GCT ATA TCA TAT GAT GGA AGT AAC AAA TAC TAT GCA GAC TCC GTG | 192 |
| Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val |     |
| 170 175 180                                                     |     |
| AAG GGC CGA TTC TCC ATC TCC AGA GAC AAT TCC AAC AAT ACG CTA TAT | 240 |
| Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr |     |
| 185 190 195 200                                                 |     |
| CTG CAA ATG AGC ACC CTG AGA GCT GAG GAC ACG GCT GTC TAT TTC TGT | 288 |
| Leu Gln Met Ser Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys |     |
| 205 210 215                                                     |     |
| GCG AGA GAT TCG GAA ACG GCA ATA GCG GCA GCT GGA CGG TTT GAT ATC | 336 |
| Ala Arg Asp Ser Glu Thr Ala Ile Ala Ala Ala Gly Arg Phe Asp Ile |     |
| 220 225 230                                                     |     |
| TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA                     | 369 |
| Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser                     |     |
| 235 240                                                         |     |

(2) INFORMATION FOR SEQ ID NO: 22:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr  
 20 25 30  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Ser Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg Asp Ser Glu Thr Ala Ile Ala Ala Ala Gly Arg Phe Asp Ile  
 100 105 110  
 Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser  
 115 120

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- 5
- (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: cDNA for mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## 15 (vii) IMMEDIATE SOURCE:

- (B) CLONE(E): AI-B18

## (viii) POSITION IN THE GENOME:

- 20
- (A) CHROMOSOME/SEGMENT: 14
  - (B) MAP POSITION: q32.3

## (ix) FEATURE:

- 25
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..366

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAG | GTG | AAA | CTG | CTC | GAG | GCG | GCT | GAG | GTG | AAG | AAG | CCT | GGG | TCC |     |
| Gln | Val | Lys | Leu | Leu | Glu | Ser | Gly | Ala | Glu | Val | Lys | Pro | Gly | Ser | 48  |
| 125 |     |     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |
| TCG | GTG | ATG | GTC | TCC | TGC | AAG | GCT | TCT | GGA | GGC | ACC | TTC | AGC | CAT |     |
| Ser | Val | Met | Val | Ser | Cys | Lys | Ala | Ser | Gly | Gly | Thr | Phe | Ser | His | 96  |
| 140 |     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |
| ACT | ATC | AGC | TGG | GTG | CGG | CAG | GCC | CCT | GGA | CAA | GGC | CTT | GAG | TGG | ATG |
| Thr | Ile | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met |
|     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 | 144 |
| GGA | GGG | ATC | ACC | CCT | ATC | TTT | GGT | ACA | GTG | AAC | TAC | GCA | CAG | AAG | TTC |
| Gly | Gly | Ile | Thr | Pro | Ile | Phe | Gly | Thr | Val | Asn | Tyr | Ala | Gln | Lys | Phe |
|     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     | 192 |
| CAG | GGC | AGA | GTC | ACC | ATT | ACC | GCG | GAC | GAA | CCC | ACG | AGC | ACA | GCC | TAC |
| Gln | Gly | Arg | Val | Thr | Ile | Thr | Ala | Asp | Glu | Pro | Thr | Ser | Thr | Ala | Tyr |
|     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     | 240 |
| ATG | GAA | CTG | AGG | AGC | CTG | ACA | TCT | GAC | GAC | TCG | GGC | ATC | TAT | TAC | TGT |
| Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Asp | Asp | Ser | Gly | Ile | Tyr | Tyr | Cys |
|     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     | 288 |
| GCG | AGA | GAA | GAT | GGC | ACT | ACA | GTA | CCA | AGT | CAA | CCC | CTT | GAG | TTC | TGG |
| Ala | Arg | Glu | Asp | Gly | Thr | Thr | Val | Pro | Ser | Gln | Pro | Leu | Glu | Phe | Trp |
| 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 336 |
| GGC | CAG | GGA | ACC | CGG | GTC | ACC | GTC | TCC | TCT |     |     |     |     |     |     |
| Gly | Gln | Gly | Thr | Arg | Val | Thr | Val | Ser | Ser |     |     |     |     |     | 366 |
|     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Lys | Leu | Leu | Glu | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | Met | Val | Ser | Cys | Lys | Ala | Ser | Gly | Gly | Thr | Phe | Ser | Ser | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ile | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Ile | Thr | Pro | Ile | Phe | Gly | Thr | Val | Asn | Tyr | Ala | Gln | Lys | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gly | Arg | Val | Thr | Ile | Thr | Ala | Asp | Glu | Pro | Thr | Ser | Thr | Ala | Tyr |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Asp | Asp | Ser | Gly | Ile | Tyr | Tyr | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Arg | Glu | Asp | Gly | Thr | Thr | Val | Pro | Ser | Gln | Pro | Leu | Glu | Phe | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gln | Gly | Thr | Arg | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

**The Black Belt**

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA for mRNA

10

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (vii) IMMEDIATE SOURCE:

15

- (B) CLONE(E): AI-B24

## (viii) POSITION IN THE GENOME:

20

- (A) CHROMOSOME/SEGMENT: 14  
 (B) MAP POSITION: q32.3

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..363

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCT GGG GGG | 48  |
| Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly     |     |
| 125 130 135                                                     |     |
| TCC CTG AGA CTC TCC TGT TCA GCC TCT GGA TTC ACC TTC AAT AAA TAT | 96  |
| Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Lys Tyr |     |
| 140 145 150                                                     |     |
| GCA ATA CAC TGG GTC CGC CAG GCT CCA GGG AAG GGA CTG GAA TAT GTT | 144 |
| Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val |     |
| 155 160 165 170                                                 |     |
| TCA GCT ATT AGT AGT AAT GGG GGT AAC ACA TAC TAC GCA GAC TCC GTG | 192 |
| Ser Ala Ile Ser Ser Asn Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val |     |
| 175 180 185                                                     |     |
| AAG GGC AGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT | 240 |
| Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr |     |
| 190 195 200                                                     |     |
| CTT CAA ATG AGC AGT CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT | 288 |
| Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys |     |
| 205 210 215                                                     |     |
| GTT AGA GGA AGT GGG AGC TAC TTA GGA TAC TAC TTT GAC TAC TGG GGC | 336 |
| Val Arg Gly Ser Gly Ser Tyr Leu Gly Tyr Tyr Phe Asp Tyr Trp Gly |     |
| 220 225 230                                                     |     |

CAG GGA ACC CTG GTC ACC GTC TCC TCA  
 Gln Gly Thr Leu Val Thr Val Ser Ser  
 235 240

363

## (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 121 base pairs  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Lys Tyr  
 20 25 30  
 Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val  
 35 40 45  
 Ser Ala Ile Ser Ser Asn Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr  
 65 70 75 80  
 Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Val Arg Gly Ser Gly Ser Tyr Leu Gly Tyr Tyr Phe Asp Tyr Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 20 (ii) MOLECULE TYPE: cDNA for mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## 25 (vii) IMMEDIATE SOURCE:

(B) CLONE(E): AI-B24

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 22

(B) MAP POSITION: q11

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTG GTG ACT CAG CCA CCC TCG GTG TCA GTG GCT CCA AGA CAG ACG GCC 48  
Val Val Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln Thr Ala  
125 130 135

ACG ATT ACC TGT GGG GGA TAC AAG ATT GGA AGT AAA AGT GTC CAC TGG 96  
Thr Ile Thr Cys Gly Gly Tyr Lys Ile Gly Ser Lys Ser Val His Trp  
140 145 150

TAC CAA CAG AAG CCA GGC CAG GCC CCT GTA TTG GTC GTC TAT GAG GAT 144  
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Glu Asp  
155 160 165

TCC TAC CGG CCC TCA GAG ATC CCT GAG CGA TTC TCT GGC TCC AAC TCT 192  
Ser Tyr Arg Pro Ser Glu Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser  
170 175 180 185

GGG AAC ATG GCC ACC CTG ACC ATC ACC GGG GTC GAA GCC GGG GAT GAG 240  
Gly Asn Met Ala Thr Leu Thr Ile Thr Gly Val Glu Ala Gly Asp Glu  
190 195 200

GCC GAC TAC TAC TGT CAG GTG TGG GAT AAT ACT AAT GAT CAG ACG ATA 288  
Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Thr Asn Asp Gln Thr Ile  
205 210 215

TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA CGT CAG CCC AAG GCT GCC 336  
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala  
220 225 230

CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT 366  
Pro Ser Val Thr Leu Phe Pro Pro Ser Ser  
235 240

15 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

- 70 -

Val Val Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln Thr Ala  
 1 5 10 15  
 Thr Ile Thr Cys Gly Gly Tyr Lys Ile Gly Ser Lys Ser Val His Trp  
 20 25 30  
 Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Glu Asp  
 35 40 45  
 Ser Tyr Arg Pro Ser Glu Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser  
 50 55 60  
 Gly Asn Met Ala Thr Leu Thr Ile Thr Gly Val Glu Ala Gly Asp Glu  
 65 70 75 80  
 Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Thr Asn Asp Gln Thr Ile  
 85 90 95  
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala  
 100 105 110  
 Pro Ser Val Thr Leu Phe Pro Pro Ser Ser  
 115 120

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA for mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (vii) IMMEDIATE SOURCE:

- (B) CLONE(E): AI-B38

## (viii) POSITION IN THE GENOME:

- (A) CHROMOSOME/SEGMENT: 14  
 (B) MAP POSITION: q32.3

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..366

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

COLLECTED FROM THE PATENT OFFICE

CAG GTG AAA CTG CTC GAG TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC 48  
 Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
 125 130 135  
 TCA GTG AAG GTC TCC TGC AAG GTT TCC GGA TAC ACC CTC ACT GAA TTA 96  
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu  
 140 145 150  
 TCC ATG CAC TGG GTG CGA CAG GCT CCT GGA AAA GGG CTT GAG TGG ATG 144  
 Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
 155 160 165 170  
 GGA GGT TTT GAT CCT GAA GAT GGT GAA ACA ATC TAC GCA CAG AAA TTC 192  
 Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe  
 175 180 185  
 CAG GGC AGA GTC ACC ATG ACC GAG GAC ACA TCT ACA GAC ACG GCC TAC 240  
 Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr  
 190 195 200  
 ATG GAG CTG AGC AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT 288  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 205 210 215  
 GAG ACA GGT CTG AGG TCG TAC AAC TAT GGT CGT AAC CTT GAC TAT TGG 336  
 Glu Thr Gly Leu Arg Ser Tyr Asn Tyr Gly Arg Asn Leu Asp Tyr Trp  
 220 225 230  
 GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA 366  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 235 240

## (2) INFORMATION FOR SEQ ID NO: 30:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu  
 20 25 30  
 Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45  
 Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe  
 50 55 60  
 Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Glu Thr Gly Leu Arg Ser Tyr Asn Tyr Gly Arg Asn Leu Asp Tyr Trp  
 100 105 110

al Thr Val  
120

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